

Fig.1

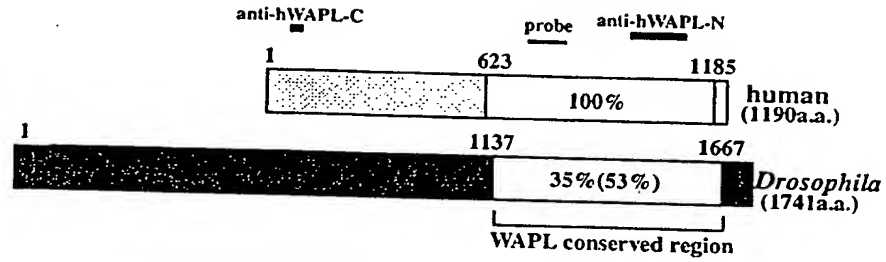


Fig. 2

hWAPL: 623 LKCRREDKELYTVVQHVKHFNDDVEFGENQEFTDDIEYLLSGLKSTQPLNTRCLSVISLA 682
 ++ R+ K+ Y VV++VK ++ E GE QE DD+EY+L L+ P TRCLS + LA
 dWAPL: 1137 IRVDRKTKDYYPVVRNVKTAHQIQEIGEYQEMDDDDVEYILDALQPHNPPATRCLSALQLA 1196

hWAPL: 683 TKCAMPSFRMHLRAHGMVAMVFKTLDDSQHHQNLSLCTAALMYILSRDRNLNMDLDRASLD 742
 KC MP+FRMH+RAHG+V FK L D+ +L LCT+A+MYILS++ LNMDLDR SL+
 dWAPL: 1197 AKCMMPAFRMHVRAHGVVTKFFKALSDANKDLSLGLCTSAIMYILSQEGLNMDLDRDSLE 1256

hWAPL: 743 LMIRLLELEQDASSAKL--LNEKDMNKIKEKIRRLCETV----HNKHLDLNITTGHLAM 796
 LMI LLE + S + + ++ K+K+R LCE + HL++++T G LAM
 dWAPL: 1257 LMINLLEADGVGGSTETGHSRAGYDRNKQKVRELCEEIKAQKGKTHLNVDLSLVGTGLAM 1316

hWAPL: 797 ETLLSLTSKRAGDWFKEELRLLGGLDHIVDKVKE-CVDHLSRDED---EKLVLASLWGAE 852
 ETLLSLTSKRAG+WFKE+LR LGGL+HI+ + + C ++ D + + L+ ++
 dWAPL: 1317 ETLLSLTSKRAGEWFKEDLRKLGGLLEHIKTIISDFCRPVIACOTEIDWQPTLLDNMQTV 1376

hWAPL: 853 RCLRVLESVTVHNPNQSYLIAKDSQLIVSSAKALQHCEELIQQYNRAEDSICLADSKP 912
 RCLRVLE+VT HN NQ Y++ + + E L Q Y I L S
 dWAPL: 1377 RCLRVLENTQHNETNQRYMLTSGQGKAV-----ETLCQLYRLCSRQIMLHPSD- 1425

hWAPL: 913 LPHQNVNTNHVGKAVEDCMRAIIGVLLNLTND-NE----WGSTKTGEQDGLIGTALNCVLQ 967
 + H G A+ + + ++ VL+NLT+ NE G+ G++ ++ T+ +L
 dWAPL: 1426 -GGGSNKEHPGVAMRELLVPVLKVLINLTHTFNEAQP SLGAELLGQRGDVVETSFRLLLL 1484

hWAPL: 968 VPKYLPQEQRFDIRVLGLGLLINLVEYSARNRHCLVNMETSCSFDSSICSGEGDSDLRIG 1027
 Y+P + F++ +L L LLINL ++ NR L+ + + D+
 dWAPL: 1485 SANYIPDQC VFELSILVLTLLINLCMHTVPNRAALMQAAAPAEYVA-----DNPPAQ 1536

hWAPL: 1028 GQVHAVQALVQLFLERERAAQLAESKTDELIKDAPTTQHDKSGEWQETSGEIQWVSTEKT 1087
 G V A+QAL++ F + E A+L E TD ++ ++K + QE E
 dWAPL: 1537 GVSALQALLEFYKCEELARLVEKNTDAFLE-----SNEKGKKKQEEVEE----- 1582

hWAPL: 1088 DGTEEKHKKEEEDDLNKLALQHAGKHMEDCIVASYTALLGCLCQESPINVTTVREYL 1147
 +N +Q AG HME + SY A+L+G L ++ + + VR L
 dWAPL: 1583 -----TVNNLVQRAGHHMEHTLKGSYAAILVGNLIADNELYESVVRRL 1626

hWAPL: 1148 PEGDFSIMTEMLKKFLSFMNLT---AVGTTGQKSISRVE 1185
 F + +L+K+ +FMNLT A KS R+I+
 dWAPL: 1627 RGNSFKEIIGVLEKYHTFMNLTSSLEAAFVAHMKSTKRIID 1667

>pir:T13610 [T13610] parallel sister chromatids protein - fruit fly
 Length = 1741

Identities = 204/581 (35%), Positives = 309/581 (53%), Gaps = 68/581 (11%)

Fig. 3

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1  MTSRFGKTYSAKGGNGSSKFOEVFSHKRTTLSTRWGSETTFMAKLCQKRPNFKPDICEIPK
1  MTSRFGKTYSAKGGNGSSKFOEVFSHKRTTLSTRWGSETTFMAKLCQKRPNFKPDICEIPK

61  KPKVEESITGDPFGFSDDESIPVSSNLAQVCSYSSESSEAAQLEEVTSVLEANSKIS
61  KPKVEEEDTGPFGFSDDESIPVSSNLAQVCSYSSESSEAAQLEEVTSVLEANSKIS

121  HVVVECTVYSEKPTTEDTLCKEKSIRIVEDASISSCKLITSDKVENFEEHEKNS
121  HVVVECTVYSEKPTTEDTLCKEKSIRIVEDASISSCKLITSDKVENFEEHEKNS

181  HHQKNAEDSTKKNPAETVASEIKETN-----DTWNSQTKKRESPEISIRKGSVRTC
181  HHQKNAEDSTKKNPAETVASEIKETN-----DTWNSQTKKRESPEISIRKGSVRTC

237  LIEWDNDFEDIRSEDICLSLGGDFLEMKDDDKN---RLLENLNEALPEEDVOSVLRKNS
241  LIEWDNDFEDIRSEDICLSLGGDFLEMKDDDKN---RLLENLNEALPEEDVOSVLRKNS

294  CRTYCRANFTLSSQCASNFDKLDGTSCLAKANSESSKDGLNQAKKQVSCGTSFRCTV
301  CRTYCRANFTLSSQCASNFDKLDGTSCLAKANSESSKDGLNQAKKQVSCGTSFRCTV

354  GATRDYTVLHPSCLSVCNVTIQDTMERSMDEFTASTPADLGEAGRLKKADIATSKTTR
361  GATRDYTVLHPSCLSVCNVTIQDTMERSMDEFTASTPADLGEAGRLKKADIATSKTTR

414  FRPSNTRSKMDVKLEFFGFEDHETCG-DECGSGSSNYKIKYFCFDLSESEDDDDDCQV
421  FRPSNTRSKMDVKLEFFGFEDHETCG-DECGSGSSNYKIKYFCFDLSESEDDDDDCQV

473  ERYTSKKRTKTAPSPSPPPESDNSQDSQSCANNAENLDFTEDLPGVPESVKKPIKSK
481  ERYTSKKRTKTAPSPSPPPESDNSQDSQSCANNAENLDFTEDLPGVPESVKKPIKSK

533  GDKSKENTRKIESGPKRSPTKAVYNARHWNHPDSEELPGPPIKPKQSVTVRLSSKEPNQK
541  GDKSKENTRKIESGPKRSPTKAVYNARHWNHPDSEELPGPPIKPKQSVTVRLSSKEPNQK

593  DDGVFKAPAPSKVIKTVTIPTQFYCIIVTALKCFEDKELYTVVQHVKKHFNQVVEFGEN
601  DDGVFKAPAPSKVIKTVTIPTQFYCIIVTALKCFEDKELYTVVQHVKKHFNQVVEFGEN

653  QEFTHDIEYLLSGLKSTQPLNTRCLSVISLATKCAMPSEFMHLRAHGMVAMVFTLDDSC
661  QEFTHDIEYLLSGLKSTQPLNTRCLSVISLATKCAMPSEFMHLRAHGMVAMVFTLDDSC

713  HHQNLSLCTAALMYILSRDRINMDLRASLDLMIIRIVLEQDASSAKLLNEKDMKIKER
721  HHQNLSLCTAALMYILSRDRINMDLRASLDLMIIRIVLEQDASSAKLLNEKDMKIKER

773  IRRLCETVHHKHLLENITGHLAMETLLSLTSKRAGDNFKEELRLGGLDHIQDKVREC
781  IRRLCETVHHKHLLENITGHLAMETLLSLTSKRAGDNFKEELRLGGLDHIQDKVREC

833  VDHLSRLDEDEKLVASLWGAERCLRVLESVTVHNPENQSYLIAYKDSQLVSSAKALQH
841  VDHLSRLDEDEKLVASLWGAERCLRVLESVTVHNPENQSYLIAYKDSQLVSSAKALQH

892  CEELICQYNRAFCSTQADSPLRCHVTNHVGFAVEDCMRAIIGVLLNLNDNEWGSK
901  CEELICQYNRAFCSTQADSPLRCHVTNHVGFAVEDCMRAIIGVLLNLNDNEWGSK

952  TGEELGLIGTNCVLQVPKYLPCQQRFDIRVLGGLLLINLVEYSARNRHCLVNNITSCS
961  TGEELGLIGTNCVLQVPKYLPCQQRFDIRVLGGLLLINLVEYSARNRHCLVNNITSCS

1012  FDSSYCSGEGD-SLRACQVHAVQALVQLFLERERAAQLAESKTDELIKDAPTTQHDKSG
1021  FDSSYCSGEGD-SLRACQVHAVQALVQLFLERERAAQLAESKTDELIKDAPTTQHDKSG

1072  EWQETSCEIQWVSTKTDGEEKKKKEEDEELDNLKALQHAGKHMEDCIVASYTALLC
1081  EWQETSCEIQWVSTKTDGEEKKKKEEDEELDNLKALQHAGKHMEDCIVASYTALLC

1132  CLCQESPINVTTVREYLFEGDPSIMTEMLKKFLSFMILTCAVGTGQKSISRVIYELHC
1141  CLCQESPINVTTVREYLFEGDPSIMTEMLKKFLSFMILTCAVGTGQKSISRVIYELHC
    
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The upper and the lower rows are the sequences of the human and the mouse WAPLs, respectively. White and gray parts indicate the same and similar amino acids, respectively. The part in the frame is a region having similarity to the *Drosophila* WAPL.

Fig. 4

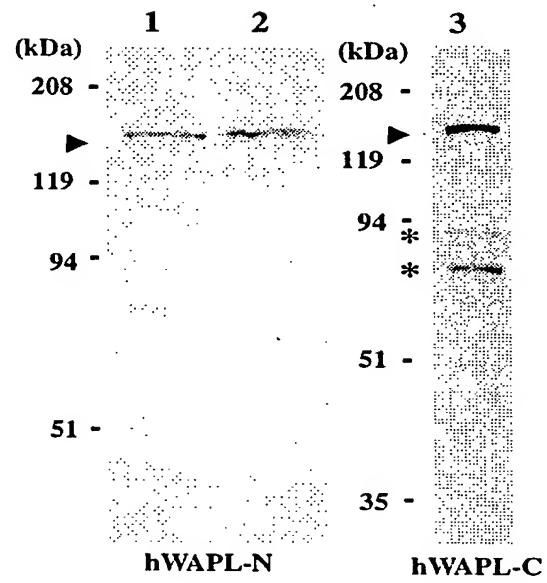


Fig.5

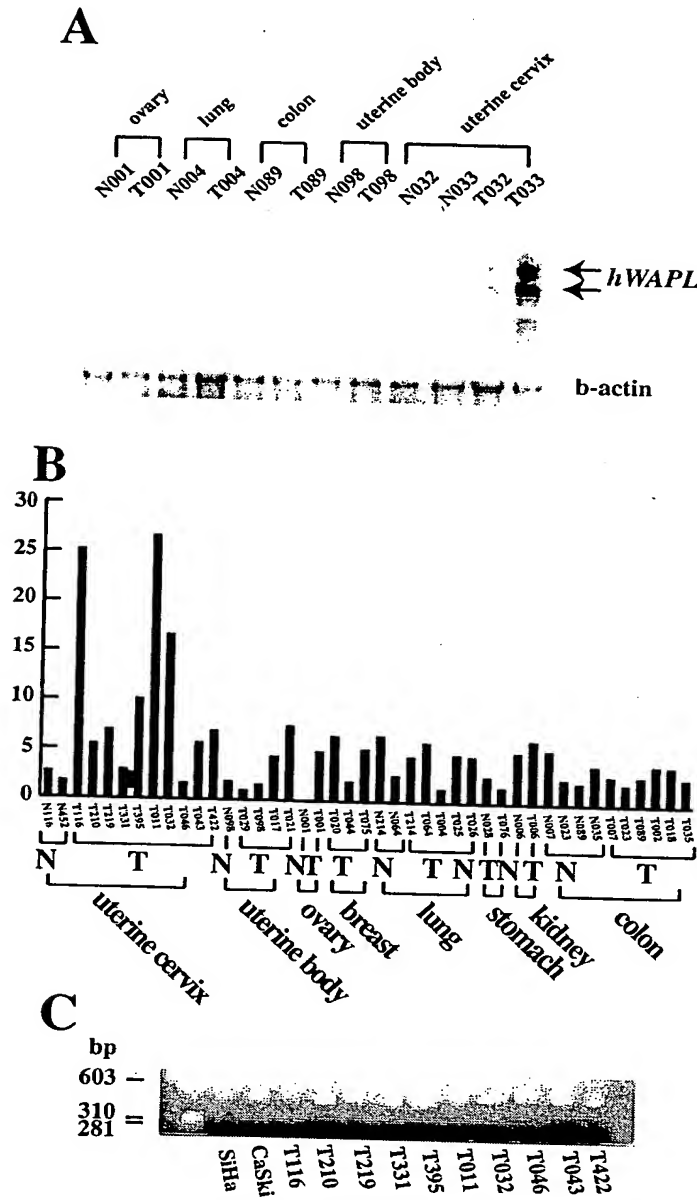
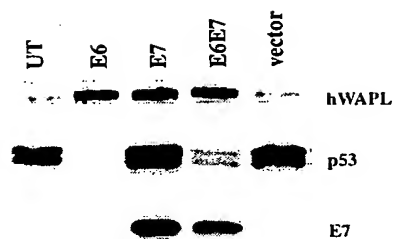


Fig. 6

A



B

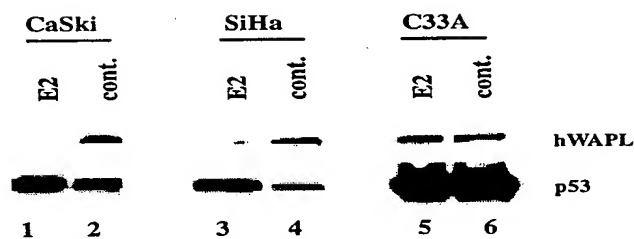
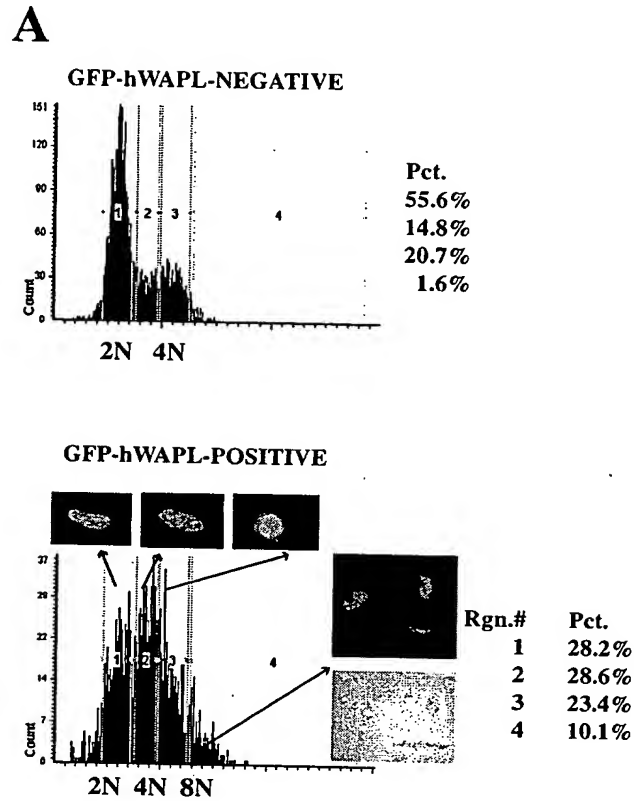


Fig. 7



B

micronuclei	+	-	total
GFP-hWAPL-NEGATIVE	60	940	1000
GFP-hWAPL-POSITIVE	124	876	1000

$p < 0.01$

Fig. 8

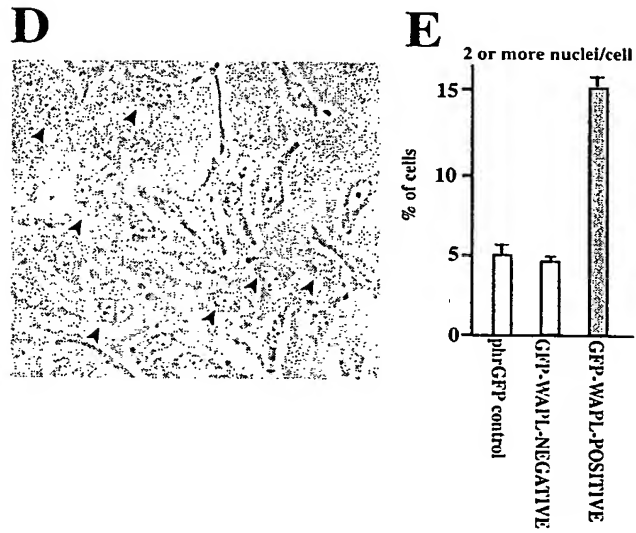
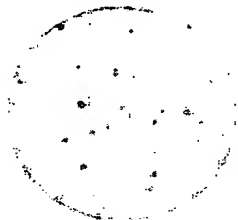


Fig. 9

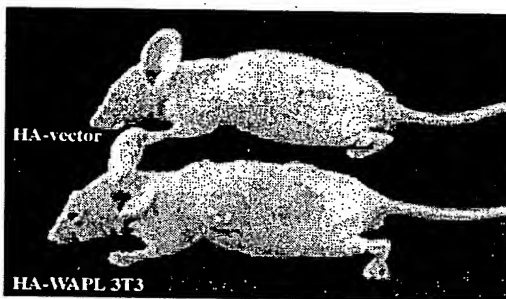
A

HA-WAPL 3T3

HA-3T3



B



C

1 2 3 4 5 6



anti-hWAPL-C



HA

D

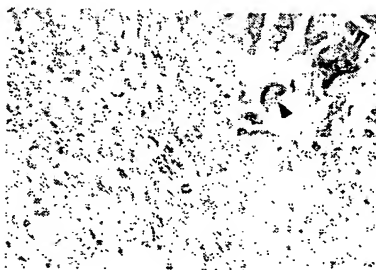


Fig.10

